FIGURE 1

1	ATGTCAGTGGGAGCCATGAAGAAGGGAGTGGGGAGGGCAGTTGGGCTTGGAGGCGGCAGC	60
61	GGCTGCCAGGCTACGGAGGAAGACCCCCTTCCCGACTGCGGGGCTTGCGCTCCGGGACAA	120
121	GGTGGCAGGCGCTGGAGGCTGCCGCAGCCTGCGTGGGTGGAGGGGAGCTCAGCTCGGTTG	180
181	TGGGAGCAGGCGACCGGCACTGGCTGGATGGACCTGGAAGCCTCGCTGCTGCCCACTGGT	240
241	CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTCAGCAGGATCACCTCCT	300
301	CGCACGGGGAGCATCTCCTACATCAACATCATCATGCCTTCGGTGTTCGGCACCATCTGC	360
361	CTCCTGGGCATCATCGGGAACTCCACGGTCATCTTCGCGGTCGTGAAGAAGTCCAAGCTG	420
421	CACTGGTGCAACAACGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTC	480
481	TTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTT	540
541	GGGGAGACCATGTGCACCCTCATCACGGCCATGGATGCCAATAGTCAGTTCACCAGCACC	600
601	TACATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCC	660
661	ACGAAGTTCCGGAAGCCCTCTGTGGCCACCCTGGTGATCTGCCTCCTGTGGGCCCTCTCC	720
721	TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCTTCCCAGGAGGTGCA	780
781	GTGGGCTGCGGCATACGCCTGCCCAACCCAGACACTGACCTCTACTGGTTCACCCTGTAC	840
841	CAGTTTTTCCTGGCCTTTGCCCTGCCTTTTGTGGTCATCACAGCCGCATACGTGAGGATC	900
901	CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCTCCCAGCGCAGCATCCGGCTGCGGACA	960
961	AAGAGGGTGACCCGCACAGCCATCGCCATCTGTCTGGTCTTCTTTGTGTGCTGGGCACCC	1020
1021	TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCCGACCCTCACCTTTGTCTAC	1080
1081	TTATACAATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTTGTGTAC	1140
1141	ATCGTGCTCTGTGAGACGTTCCGCAAACGCTTGGTCCTGTCGGTGAAGCCTGCAGCCCAG	1200
1201	GGGCAGCTTCGCGCTGTCAGCAACGCTCAGACGGCTGACGAGGAGAGGACAGAAAGCAAA	1260
1261	GGCACCTGA	1269

FIGURE 2

```
  1  M S V G A M K K G V G R A V G L G G G S   20
 21  G C Q A T E E D P L P D C G A C A P G Q   40
 41  G G R R W R L P Q P A W V E G S S A R L   60
 61  W E Q A T G T G W M D L E A S L L P T G   80
 81  P N A S N T S D G P D N L T S A G S P P  100
101  R T G S I S Y I N I I M P S V F G T I C  120
121  L L G I I G N S T V I F A V V K K S K L  140
141  H W C N N V P D I F I I N L S V V D L L  160
161  F L L G M P F M I H Q L M G N G V W H F  180
181  G E T M C T L I T A M D A N S Q F T S T  200
201  Y I L T A M A I D R Y L A T V H P I S S  220
221  T K F R K P S V A T L V I C L L W A L S  240
241  F I S I T P V W L Y A R L I P F P G G A  260
261  V G C G I R L P N P D T D L Y W F T L Y  280
281  Q F F L A F A L P F V V I T A A Y V R I  300
301  L Q R M T S S V A P A S Q R S I R L R T  320
321  K R V T R T A I A I C L V F F V C W A P  340
341  Y Y V L Q L T Q L S I S R P T L T F V Y  360
361  L Y N A A I S L G Y A N S C L N P F V Y  380
381  I V L C E T F R K R L V L S V K P A A Q  400
401  G Q L R A V S N A Q T A D E E R T E S K  420
421  G T                                      422
```

FIGURE 3

```
  1  M S V G A M K K G V G R A V G L G G G S  20
 21  G C Q A T E E D P L P D C G A C A P G Q  40
 41  G G R R W R L P Q P A W V E G S S A R L  60
 61  W E Q A T G T G W M D L E A S L L P T G  80
 81  P N A S N T S D G P D N L T S A G S P P 100
101  R T G S I S Y I N I I M P S V F G T I C 120
                I
121  L I G I I G N S T V I F A V V K K S K L 140
                                     II
141  H W C N N V P D I F I I N L S V V D L L 160
161  F L L G M P F M I H Q L M G N G V W H F 180
181  G E T M C T L I T A M D A N S Q F T S T 200
               III
201  Y I L T A M A I D R Y L A T V H P I S S 220
221  T K F R K P S V A T L V I C I L W A L S 240
                          IV
241  F I S I T P V W L Y A R L I P F P G G A 260
261  V G C G I R L P N P D T D L Y W F T L Y 280
                      V
281  Q F F L A F A L P F V V I T A A Y V R I 300
301  L Q R M T S S V A P A S Q R S I R L R T 320
                                  VI
321  K R V T R T A I A I C L V F F V C W A P 340
341  Y Y V L Q L T Q L S I S R P T L T F V Y 360
                        VII
361  L Y N A A I S L G Y A N S C L N P F V Y 380
381  I V L C E T F R K R L V L S V K P A A Q 400
401  G Q L R A V S N A Q T A D E E R T E S K 420
                                           422
421  G T
```

FIGURE 4

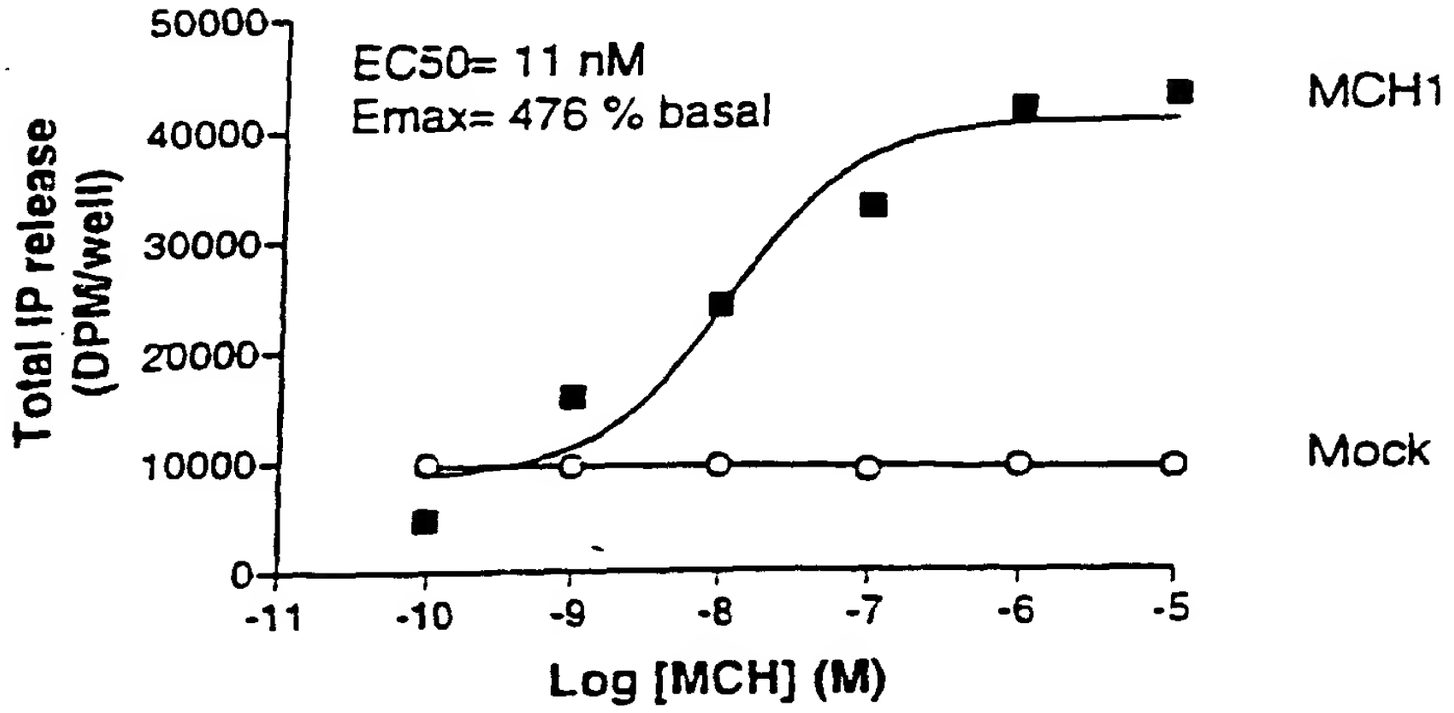
```
1     GCAGGCGACCTGCACCGGCTGCATGGATCTGCAAACCTCGTTGCTGTCCACTGGCCCCAA   60
61    TGCCAGCAACATCTCCGATGGCCAGGATAATCTCACATTGCCGGGGTCACCTCCTCGCAC   120
121   AGGGAGTGTCTCCTACATCAACATCATTATGCCTTCCGTGTTTGGTACCATCTGTCTCCT   180
181   GGGCATCGTGGGAAACTCCACGGTCATCTTTGCTGTGGTGAAGAAGTCCAAGCTACACTG   240
241   GTGCAGCAACGTCCCCGACATCTTCATCATCAACCTCTCTGTGGTGGATCTGCTCTTCCT   300
301   GCTGGGCATGCCTTTCATGATCCACCAGCTCATGGGGAACGGCGTCTGGCACTTTGGGGA   360
361   AACCATGTGCACCCTCATCACAGCCATGGACGCCAACAGTCAGTTCACTAGCACCTACAT   420
421   CCTGACTGCCATGACCATTGACCGCTACTTGGCCACCGTCCACCCCATCTCCTCCACCAA   480
481   GTTCCGGAAGCCCTCCATGGCCACCCTGGTGATCTGCCTCCTGTGGGCGCTCTCCTTCAT   540
541   CAGTATCACCCCTGTGTGGCTCTACGCCAGGCTCATTCCCTTCCCAGGGGGTGCTGTGGG   600
601   CTGTGGCATCCGCCTGCCAAACCCGGACACTGACCTCTACTGGTTCACTCTGTACCAGTT   660
661   TTTCCTGGCCTTTGCCCTTCCGTTTGTGGTCATTACCGCCGCATACGTGAAAATACTACA   720
721   GCGCATGACGTCTTCGGTGGCCCCAGCCTCCCAACGCAGCATCCGGCTTCGGACAAAGAG   780
781   GGTGACCCGCACGGCCATTGCCATCTGTCTGGTCTTCTTTGTGTGCTGGGCACCCTACTA   840
841   TGTGCTGCAGCTGACCCAGCTGTCCATCAGCCGCCCGACCCTCACGTTTGTCTACTTGTA   900
901   CAACGCGGCCATCAGCTTGGGCTATGCTAACAGCTGCCTGAACCCCTTTGTGTACATAGT   960
961   GCTCTGTGAGACCTTTCGAAAACGCTTGGTGTTGTCAGTGAAGCCTGCAGCCCAGGGGCA   1020
1021  GCTCCGCACGGTCAGCAACGCTCAGACAGCTGATGAGGAGAGGACAGAAAGCAAAGGCAC   1080
1081  CTGACAATTCCCCAGTCGCCTCCAAGTCAGGCCACCCCATCAAACCGTGGGGAGAGATAC   1140
1141  TGAGATTAAACCCAAGGCTACCCTGGGAGAATGCAGAGGCTGGAGGCTGGGGGCTTGTAG   1200
1201  CAACCACATTCCAC                                                 1214
```

FIGURE 5

1	M	D	L	Q	T	S	L	L	S	T	G	P	N	A	S	N	I	S	D	G	20
21	Q	D	N	L	T	L	P	G	S	P	P	R	T	G	S	V	S	Y	I	N	40
41	I	I	M	P	S	V	F	G	T	I	C	L	L	G	I	V	G	N	S	T	60
61	V	I	F	A	V	V	K	K	S	K	L	H	W	C	S	N	V	P	D	I	80
81	F	I	I	N	L	S	V	V	D	L	L	F	L	L	G	M	P	F	M	I	100
101	H	Q	L	M	G	N	G	V	W	H	F	G	E	T	M	C	T	L	I	T	120
121	A	M	D	A	N	S	Q	F	T	S	T	Y	I	L	T	A	M	T	I	D	140
141	R	Y	L	A	T	V	H	P	I	S	S	T	K	F	R	K	P	S	M	A	160
161	T	L	V	I	C	L	L	W	A	L	S	F	I	S	I	T	P	V	W	L	180
181	Y	A	R	L	I	P	F	P	G	G	A	V	G	C	G	I	R	L	P	N	200
201	P	D	T	D	L	Y	W	F	T	L	Y	Q	F	F	L	A	F	A	L	P	220
221	F	V	V	I	T	A	A	Y	V	K	I	L	Q	R	M	T	S	S	V	A	240
241	P	A	S	Q	R	S	I	R	L	R	T	K	R	V	T	R	T	A	I	A	260
261	I	C	L	V	F	F	V	C	W	A	P	Y	Y	V	L	Q	L	T	Q	L	280
281	S	I	S	R	P	T	L	T	F	V	Y	L	Y	N	A	A	I	S	L	G	300
301	Y	A	N	S	C	L	N	P	F	V	Y	I	V	L	C	E	T	F	R	K	320
321	R	L	V	L	S	V	K	P	A	A	Q	G	Q	L	R	T	V	S	N	A	340
341	Q	T	A	D	E	E	R	T	E	S	K	G	T	*							354

FIGURE 6

IP release in MCH1- and mock-transfected Cos-7 cells



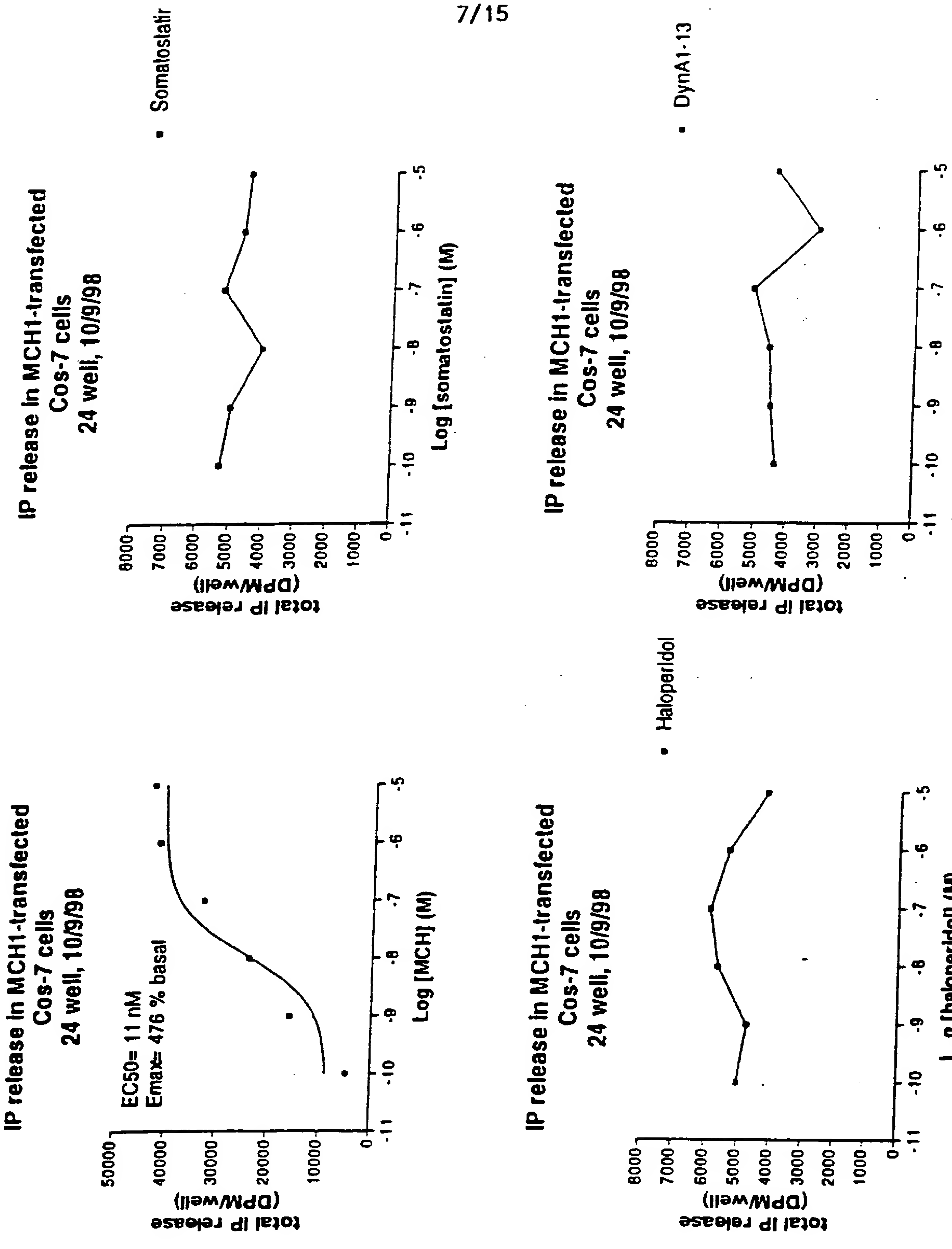

IP release in MCH1-transfected
Cos-7 cells
24 well, 10/9/98
Somatostatin
total IP release (DPM/well)
Log [somatostatin] (M)
IP release in MCH1-transfected
Cos-7 cells
24 well, 10/9/98
DynA1-13
total IP release (DPM/well)
Log [Dyn-A- 1-13] (M)
IP release in MCH1-transfected
Cos-7 cells
24 well, 10/9/98
EC50= 11 nM
Emax= 476 % basal
total IP release (DPM/well)
Log [MCH] (M)
IP release in MCH1-transfected
Cos-7 cells
24 well, 10/9/98
Haloperidol
total IP release (DPM/well)
L g [haloperidol] (M)

FIGURE 7

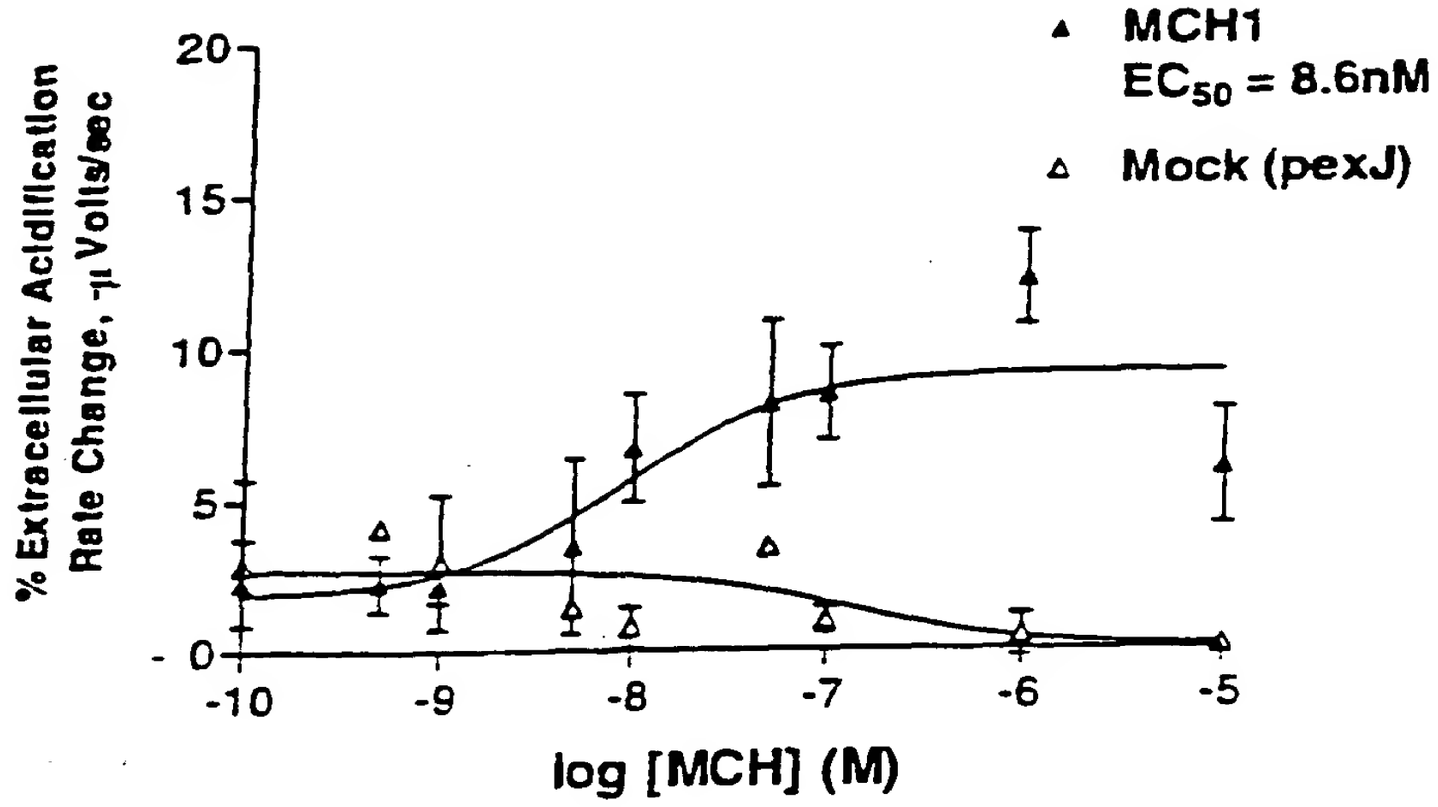

Microphysiometer Response
CHO cells
MCH1
EC50 = 8.6nM
Mock (pexJ)
% Extracellular Acidification Rate Change, -µ Volts/sec
20
15
10
5
0
-10
-9
-8
-7
-6
-5
log [MCH] (M)

FIGURE 8

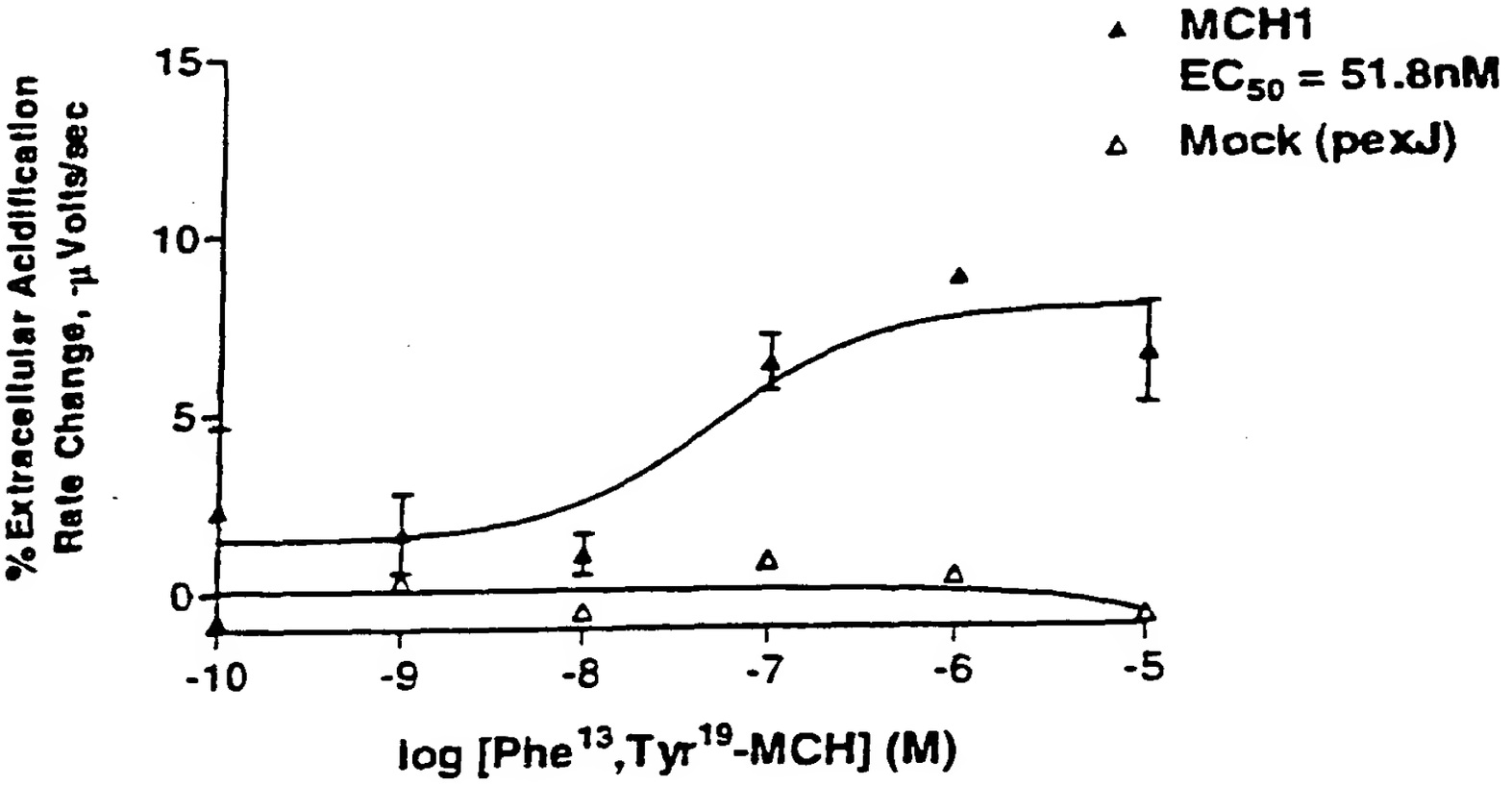

Microphysiometer Response
CHO cells
MCH1
EC50 = 51.8nM
Mock (pexJ)
% Extracellular Acidification Rate Change, -µ Volts/sec
15
10
5
0
-10
-9
-8
-7
-6
-5
log [Phe13,Tyr19-MCH] (M)

FIGURE 9

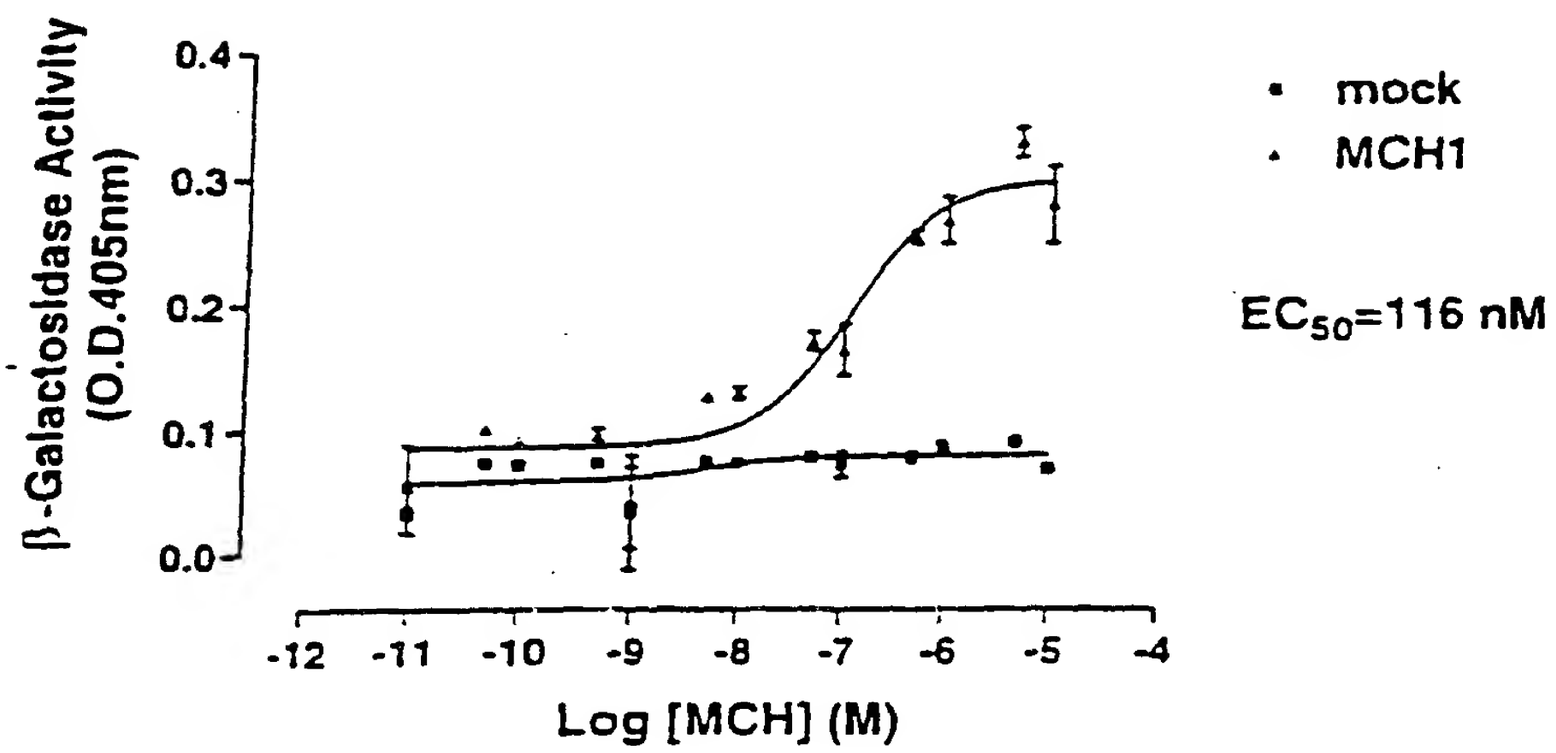
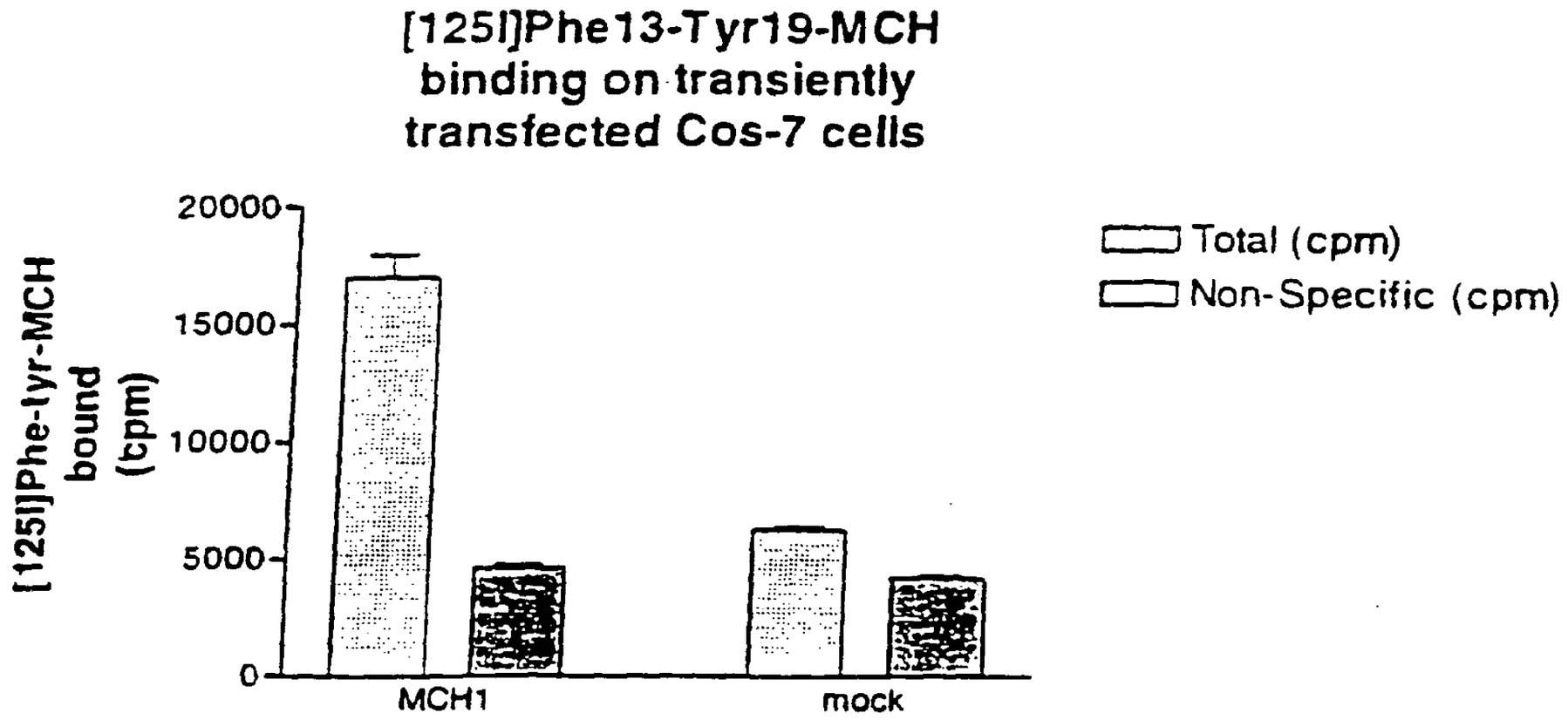

Agonist-Mediated c-fos-β-gal
Activity in Cos-7 Cells
β-Galactosidase Activity
(O.D.405nm)
0.4
0.3
0.2
0.1
0.0
-12
-11
-10
-9
-8
-7
-6
-5
-4
Log [MCH] (M)
mock
MCH1
EC50=116 nM

FIGURE 10



[125I]Phe13-Tyr19-MCH
binding on transiently
transfected Cos-7 cells

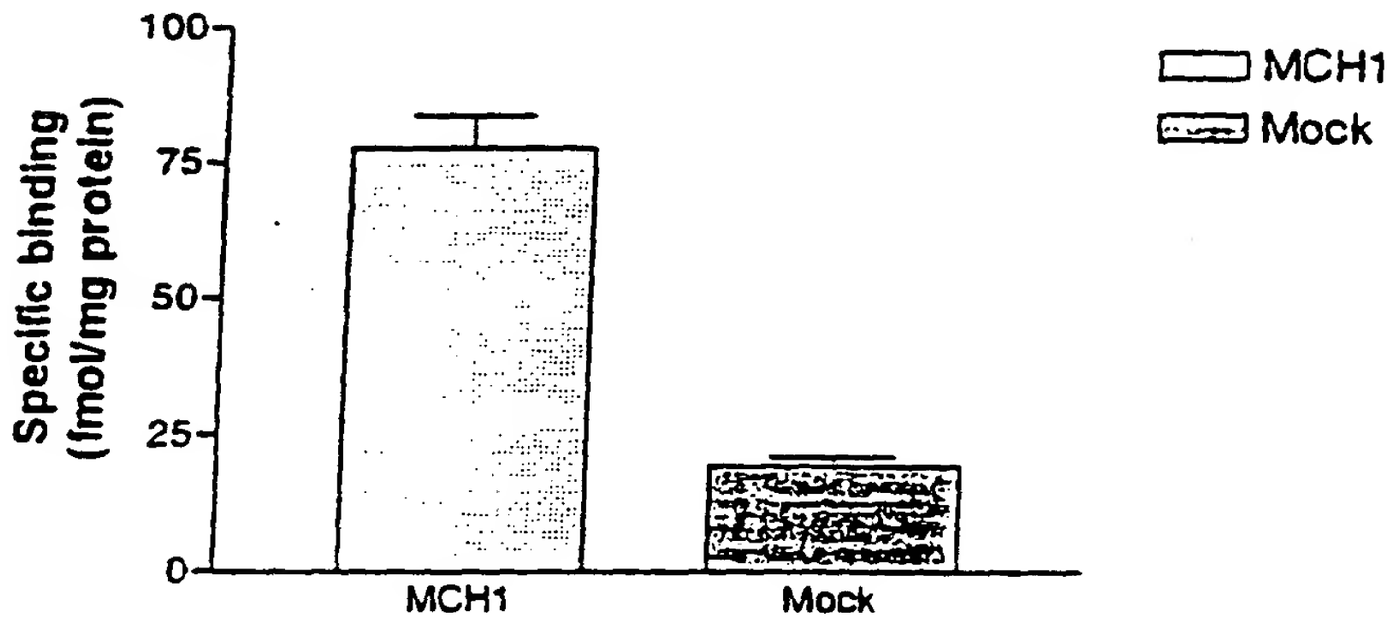


FIGURE 11

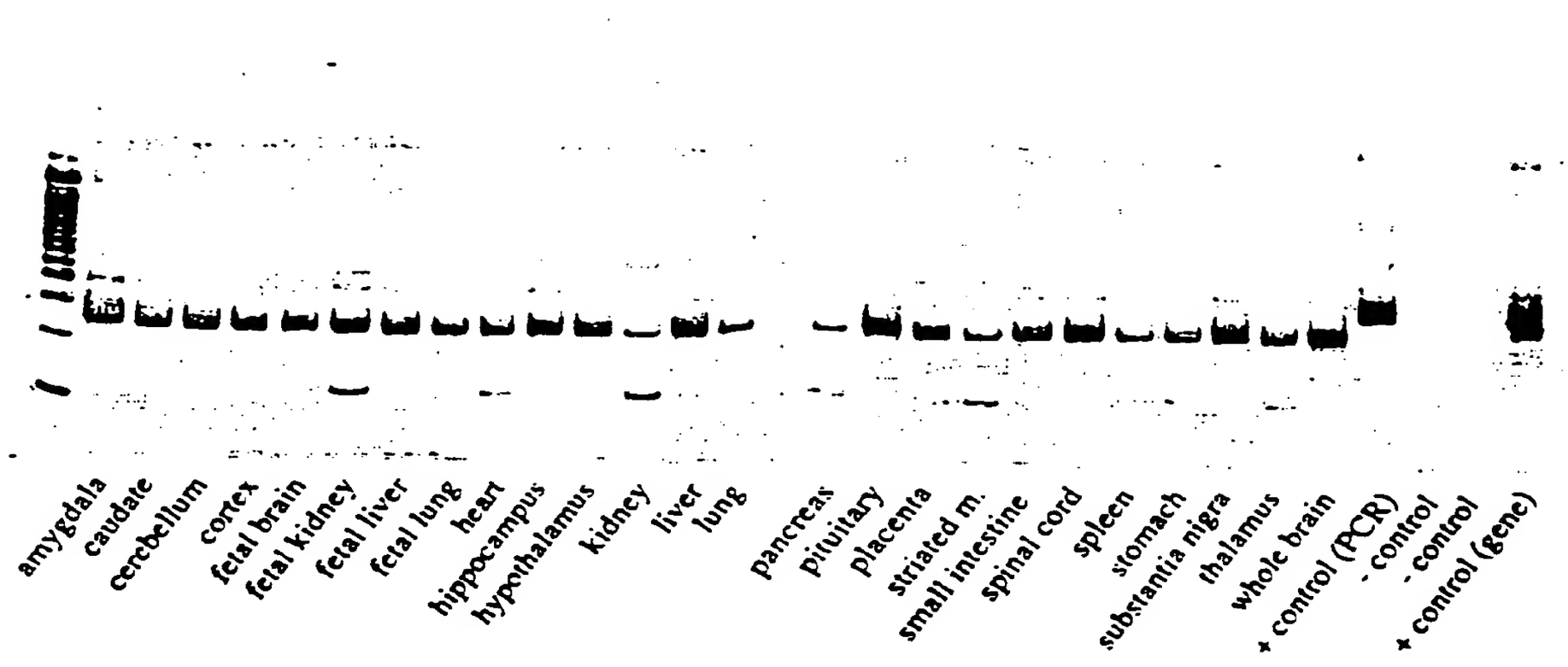

amygdala
caudate
cerebellum
cortex
fetal brain
fetal kidney
fetal liver
fetal lung
heart
hippocampus
hypothalamus
kidney
liver
lung
pancreas
pituitary
placenta
striated m.
small intestine
spinal cord
spleen
stomach
substantia nigra
thalamus
whole brain
+ control (PCR)
- control
- control
+ control (gene)

Figure 12

```
                1                                                   40
TL231           MSVGAMKKGV   GRAVGLGGGS   GCQATEEDPL PDCGACAPGQ
R106            MSVGAMKKGV   GRAVGLGGGS   GCQATEEDPL PDCGACAPGQ
R114            MSVGAaKKGV   GRAVGLGGGS   GCQATEEDPL PDCGACAPGQ
BO120           ~~~~~~~~~~   ~~~~~~~~~~   ~~~~~~~~~~ ~~~~~~~~~~

               41                                                   80
TL231           GGRRWRLPQP   AWVEGSSARL   WEQATGTGWM DLEASLLPTG
R106            GGRRWRLPQP   AWVEGSSARL   WEQATGTGWa DLEASLLPTG
R114            GGRRWRLPQP   AWVEGSSARL   WEQATGTGWa DLEASLLPTG
BO120           ~~~~~~~~~~   ~~~~~~~~~~   ~~~~~~~~~~M DLEASLLPTG

               81                    100
TL231           PNASNTSDGP   DNLTSAGSPP...
R106            PNASNTSDGP   DNLTSAGSPP...
R114            PNASNTSDGP   DNLTSAGSPP...
BO120           PNASNTSDGP   DNLTSAGSPP...
```

1	M S V G A M K K G V G R A V G L G G G S	20
21	G C Q A T E E D P L P D C G A C A P G Q	40
41	G G R R W R L P Q P A W V E G S S A R L	60
61	W E Q A T G T G W A D L E A S L L P T G	80
81	P N A S N T S D G P D N L T S A G S P P	100
101	R T G S I S Y I N I I M P S V F G T I C	120
121	L L G I I G N S T V I F A V V K K S K L	140
141	H W C N N V P D I F I I N L S V V D L L	160
161	F L L G M P F M I H Q L M G N G V W H F	180
181	G E T M C T L I T A M D A N S Q F T S T	200
201	Y I L T A M A I D R Y L A T V H P I S S	220
221	T K F R K P S V A T L V I C L L W A L S	240
241	F I S I T P V W L Y A R L I P F P G G A	260
261	V G C G I R L P N P D T D L Y W F T L Y	280
281	Q F F L A F A L P F V V I T A A Y V R I	300
301	L Q R M T S S V A P A S Q R S I R L R T	320
321	K R V T R T A I A I C L V F F V C W A P	340
341	Y Y V L Q L T Q L S I S R P T L T F V Y	360
361	L Y N A A I S L G Y A N S C L N P F V Y	380
381	I V L C E T F R K R L V L S V K P A A Q	400
401	G Q L R A V S N A Q T A D E E R T E S K	420
421	G T	422

```
  1  M S V G A A K K G V G R A V G L G G G S   20
 21  G C Q A T E E D P L P D C G A C A P G Q   40
 41  G G R R W R L P Q P A W V E G S S A R L   60
 61  W E Q A T G T G W A D L E A S L L P T G   80
 81  P N A S N T S D G P D N L T S A G S P P  100
101  R T G S I S Y I N I I M P S V F G T I C  120
121  L L G I I G N S T V I F A V V K K S K L  140
141  H W C N N V P D I F I I N L S V V D L L  160
161  F L L G M P F M I H Q L M G N G V W H F  180
181  G E T M C T L I T A M D A N S Q F T S T  200
201  Y I L T A M A I D R Y L A T V H P I S S  220
221  T K F R K P S V A T L V I C L L W A L S  240
241  F I S I T P V W L Y A R L I P F P G G A  260
261  V G C G I R L P N P D T D L Y W F T L Y  280
281  Q F F L A F A L P F V V I T A A Y V R I  300
301  L Q R M T S S V A P A S Q R S I R L R T  320
321  K R V T R T A I A I C L V F F V C W A P  340
341  Y Y V L Q L T Q L S I S R P T L T F V Y  360
361  L Y N A A I S L G Y A N S C L N P F V Y  380
381  I V L C E T F R K R L V L S V K P A A Q  400
401  G Q L R A V S N A Q T A D E E R T E S K  420
421  G T                                     422
```

1	M	D	L	E	A	S	L	L	P	T	G	P	N	A	S	N	T	S	D	G	20
21	P	D	N	L	T	S	A	G	S	P	P	R	T	G	S	I	S	Y	I	N	40
41	I	I	M	P	S	V	F	G	T	I	C	L	L	G	I	I	G	N	S	T	60
61	V	I	F	A	V	V	K	K	S	K	L	H	W	C	N	N	V	P	D	I	80
81	F	I	I	N	L	S	V	V	D	L	L	F	L	L	G	M	P	F	M	I	100
101	H	Q	L	M	G	N	G	V	W	H	F	G	E	T	M	C	T	L	I	T	120
121	A	M	D	A	N	S	Q	F	T	S	T	Y	I	L	T	A	M	A	I	D	140
141	R	Y	L	A	T	V	H	P	I	S	S	T	K	F	R	K	P	S	V	A	160
161	T	L	V	I	C	L	L	W	A	L	S	F	I	S	I	T	P	V	W	L	180
181	Y	A	R	L	I	P	F	P	G	G	A	V	G	C	G	I	R	L	P	N	200
201	P	D	T	D	L	Y	W	F	T	L	Y	Q	F	F	L	A	F	A	L	P	220
221	F	V	V	I	T	A	A	Y	V	R	I	L	Q	R	M	T	S	S	V	A	240
241	P	A	S	Q	R	S	I	R	L	R	T	K	R	V	T	R	T	A	I	A	260
261	I	C	L	V	F	F	V	C	W	A	P	Y	Y	V	L	Q	L	T	Q	L	280
281	S	I	S	R	P	T	L	T	F	V	Y	L	Y	N	A	A	I	S	L	G	300
301	Y	A	N	S	C	L	N	P	F	V	Y	I	V	L	C	E	T	F	R	K	320
321	R	L	V	L	S	V	K	P	A	A	Q	G	Q	L	R	A	V	S	N	A	340
341	Q	T	A	D	E	E	R	T	E	S	K	G	T								353